



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Weeks, Donald P.  
Wang, Xiao-Zhuo  
Herman, Patricia L.
- (ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND  
USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS"
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Sheridan Ross P.C.
  - (B) STREET: 1700 Lincoln St., Suite 3500
  - (C) CITY: Denver
  - (D) STATE: Colorado
  - (E) COUNTRY: USA
  - (F) ZIP: 80203
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/042,666
  - (B) FILING DATE: 04-APR-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/042,941
  - (B) FILING DATE: 04-APR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Crook, Wannell M.
  - (B) REGISTRATION NUMBER: 31,071
  - (C) REFERENCE/DOCKET NUMBER: 3553-18
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (303) 863-9700
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

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GROUP 1800

(ix) FEATURE:  
 (A) NAME/KEY: Region  
 (B) LOCATION: 28  
 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Asp or Thr"

(ix) FEATURE:  
 (A) NAME/KEY: Region  
 (B) LOCATION: 29  
 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Pro"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu Leu  
 1                    5                    10                    15  
 Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Xaa Xaa  
                   20                    25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
 (A) NAME/KEY: Region  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:  
 (A) NAME/KEY: Region  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:  
 (A) NAME/KEY: Region  
 (B) LOCATION: 16  
 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:  
 (A) NAME/KEY: Region  
 (B) LOCATION: 20  
 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Tyr Val Val Thr Asp Ala Xaa Ile Lys Xaa Lys Tyr Met Asp Xaa  
 1                    5                    10                    15  
 Val Glu Val Xaa  
                   20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG ACC TTC GTC CGC AAT GCC TGG TAT GTG GCG GCG CTG CCC GAG GAA	48
Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu	
1 5 10 15	
CTG TCC GAA AAG CCG CTC GGC CGG ACG ATT CTC GAC ACA CCG CTC GCG	96
Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala	
20 25 30	
CTC TAC CGC CAG CCC GAC GGT GTG GTC GCG GCG CTG CTC GAC ATC TGT	144
Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys	
35 40 45	
CCG CAC CGC TTC GCG CCG CTG AGC GAC GGC ATC CTC GTC AAC GGC CAT	192
Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His	
50 55 60	
CTC CAA TGC CCC TAT CAC GGG CTG GAA TTC GAT GGC GGC GGC CAG TGC	240
Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys	
65 70 75 80	
GTC CAT AAC CCG CAC GGC AAT GGC GCC CGC CCG GCT TCG CTC AAC GTC	288
Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val	
85 90 95	
CGC TCC TTC CCG GTG GTG GAG CGC GAC GCG CTG ATC TGG ATC TGG CCC	336
Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro	
100 105 110	
GGC GAT CCG GCG CTG GCC GAT CCT GGG GCG ATC CCC GAC TTC GGC TGC	384
Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys	
115 120 125	
CGC GTC GAT CCC GCC TAT CGG ACC GTC GGC GGC TAT GGG CAT GTC GAC	432
Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp	
130 135 140	
TGC AAC TAC AAG CTG CTG GTC GAC AAC CTG ATG GAC CTC GGC CAC GCC	480
Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala	
145 150 155 160	
CAA TAT GTC CAT CGC GCC AAC GCC CAG ACC GAC GCC TTC GAC CGG CTG	528

Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu	
165 170 175	
GAG CGC GAG GTG ATC GTC GGC GAC GGT GAG ATA CAG GCG CTG ATG AAG	576
Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys	
180 185 190	
ATT CCC GGC GGC ACG CCG AGC GTG CTG ATG GCC AAG TTC CTG CCG GGC	624
Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly	
195 200 205	
GCC AAT ACC CCC GTC GAC GCT TGG AAC GAC ATC CGC TGG AAC AAG GTG	672
Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val	
210 215 220	
AGC GCG ATG CTC AAC TTC ATC GCG GTG GCG CCG GAA GGC ACC CCG AAG	720
Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys	
225 230 235 240	
GAG CAG AGC ATC CAC TCG CGC GGT ACC CAT ATC CTG ACC CCC GAG ACG	768
Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr	
245 250 255	
GAG GCG AGC TGC CAT TAT TTC TTC GGC TCC TCG CGC AAT TTC GGC ATC	816
Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile	
260 265 270	
GAC GAT CCG GAG ATG GAC GGC GTG CTG CGC AGC TGG CAG GCT CAG GCG	864
Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala	
275 280 285	
CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC CGC	912
Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg	
290 295 300	
GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC	960
Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp	
305 310 315 320	
GAA GCC GCA GTC CGT GTC AGC CGC GAG ATC GAG AAG CTT GAG CAG CTC	1008
Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu	
325 330 335	
GAA GCC GCC TGA	1020
Glu Ala Ala *	
340	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu  
 1 5 10 15  
 Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala  
 20 25 30  
 Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys  
 35 40 45  
 Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His  
 50 55 60  
 Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys  
 65 70 75 80  
 Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val  
 85 90 95  
 Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro  
 100 105 110  
 Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys  
 115 120 125  
 Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp  
 130 135 140  
 Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala  
 145 150 155 160  
 Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu  
 165 170 175  
 Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys  
 180 185 190  
 Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly  
 195 200 205  
 Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val  
 210 215 220  
 Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys  
 225 230 235 240  
 Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr  
 245 250 255  
 Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile  
 260 265 270  
 Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala  
 275 280 285  
 Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg  
 290 295 300  
 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp  
 305 310 315 320

Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu  
325 330 335

Glu Ala Ala \*  
340

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG ACC TAT GTC GTC ACC GAC GCC TGC ATC AAG TGC AAG TAC ATG GAC	48
Met Thr Tyr Val Val Thr Asp Ala Cys Ile Lys Cys Lys Tyr Met Asp	
1 5 10 15	
TGC GTG GAA GTC TGC CCT GTG GAC TGC TTC TAC GAA GGC GAG AAC ATG	96
Cys Val Glu Val Cys Pro Val Asp Cys Phe Tyr Glu Gly Glu Asn Met	
20 25 30	
CTC GTC ATC AAT CCC AGT GAA TGC ATC GAC TGC GGC GTC TGC GAA CCG	144
Leu Val Ile Asn Pro Ser Glu Cys Ile Asp Cys Gly Val Cys Glu Pro	
35 40 45	
GAA TGC CCA GCC GAA GCC ATC CTT CCC GAC ACC GAA AGC GGT CTC GAG	192
Glu Cys Pro Ala Glu Ala Ile Leu Pro Asp Thr Glu Ser Gly Leu Glu	
50 55 60	
CAG TGG ATG GAA CTG AAC ACG AAG TAC TCG GCC GAG TGG CCG AAT CTC	240
Gln Trp Met Glu Leu Asn Thr Lys Tyr Ser Ala Glu Trp Pro Asn Leu	
65 70 75 80	
ACG TCC AAG AAA GAT TCG CCG GAA GAT GCC GAC GAG TAC AAG GGC GTG	288
Thr Ser Lys Lys Asp Ser Pro Glu Asp Ala Asp Glu Tyr Lys Gly Val	
85 90 95	
GAA GGC AAG TTC GAG AAG TTC TTC TCG CCC GAG CCC GGC GAG GGC GAC	336
Glu Gly Lys Phe Glu Lys Phe Phe Ser Pro Glu Pro Gly Glu Gly Asp	
100 105 110	
TGA	339
*	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Thr	Tyr	Val	Val	Thr	Asp	Ala	Cys	Ile	Lys	Cys	Lys	Tyr	Met	Asp
1				5					10					15	
Cys	Val	Glu	Val	Cys	Pro	Val	Asp	Cys	Phe	Tyr	Glu	Gly	Glu	Asn	Met
			20					25					30		
Leu	Val	Ile	Asn	Pro	Ser	Glu	Cys	Ile	Asp	Cys	Gly	Val	Cys	Glu	Pro
			35					40					45		
Glu	Cys	Pro	Ala	Glu	Ala	Ile	Leu	Pro	Asp	Thr	Glu	Ser	Gly	Leu	Glu
	50					55					60				
Gln	Trp	Met	Glu	Leu	Asn	Thr	Lys	Tyr	Ser	Ala	Glu	Trp	Pro	Asn	Leu
65					70					75				80	
Thr	Ser	Lys	Lys	Asp	Ser	Pro	Glu	Asp	Ala	Asp	Glu	Tyr	Lys	Gly	Val
				85					90					95	
Glu	Gly	Lys	Phe	Glu	Lys	Phe	Phe	Ser	Pro	Glu	Pro	Gly	Glu	Gly	Asp
			100					105					110		

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